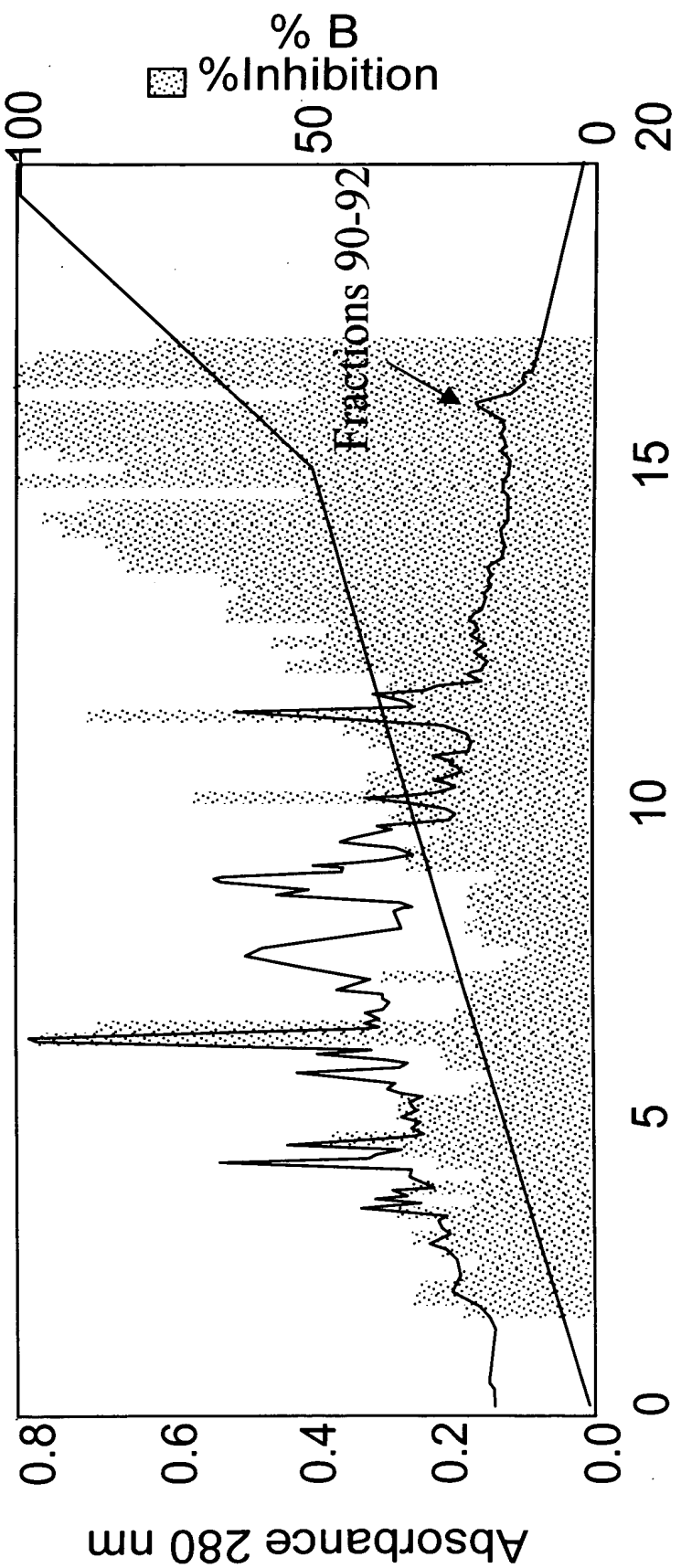
% B
%Inhibition
100
50
0
20
15
10
5
0
Hours
Fractions 90-92
0.8
0.6
0.4
0.2
0.0
Absorbance 280 nm

Fig. 1

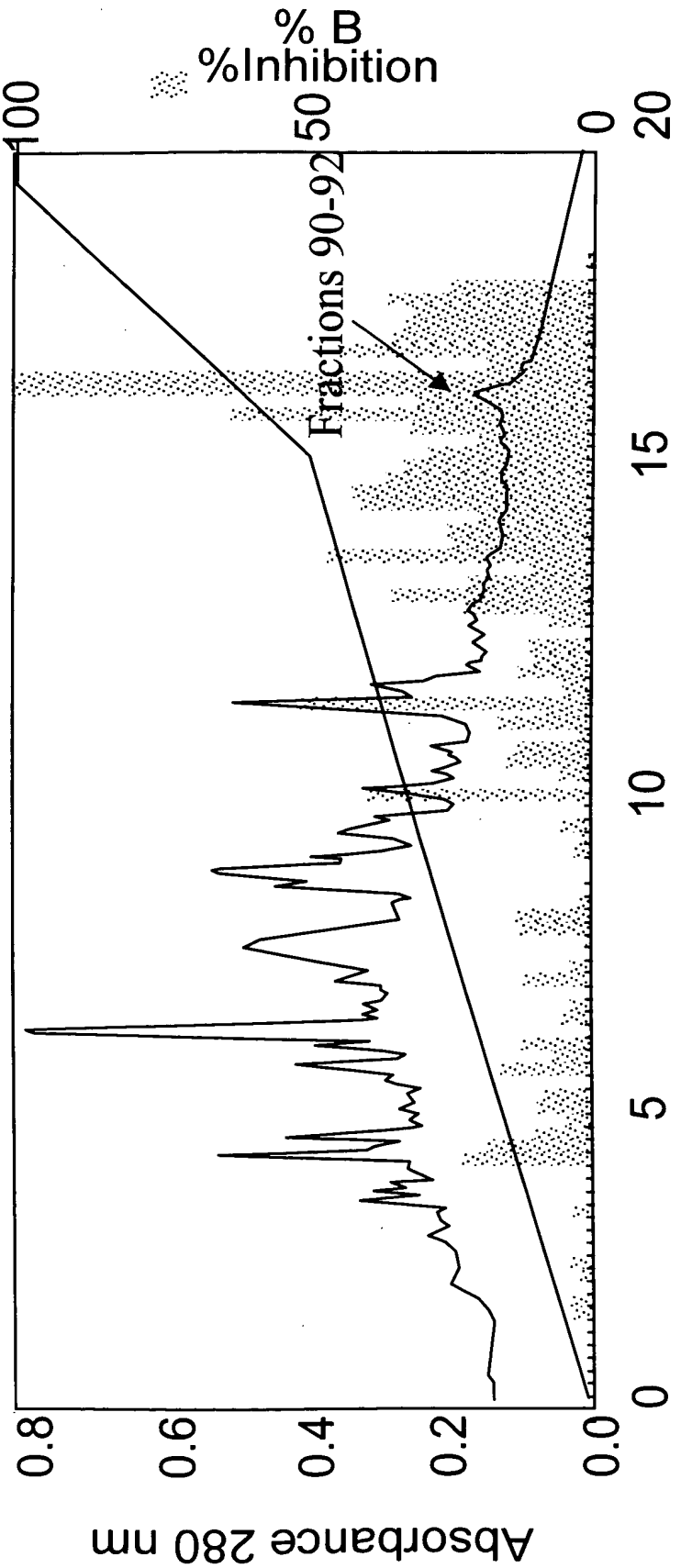
% B
%Inhibition
100
50
0
20
15
10
5
0
Hours
Fractions 90-92
0.8
0.6
0.4
0.2
0.0
Absorbance 280 nm

Fig. 2

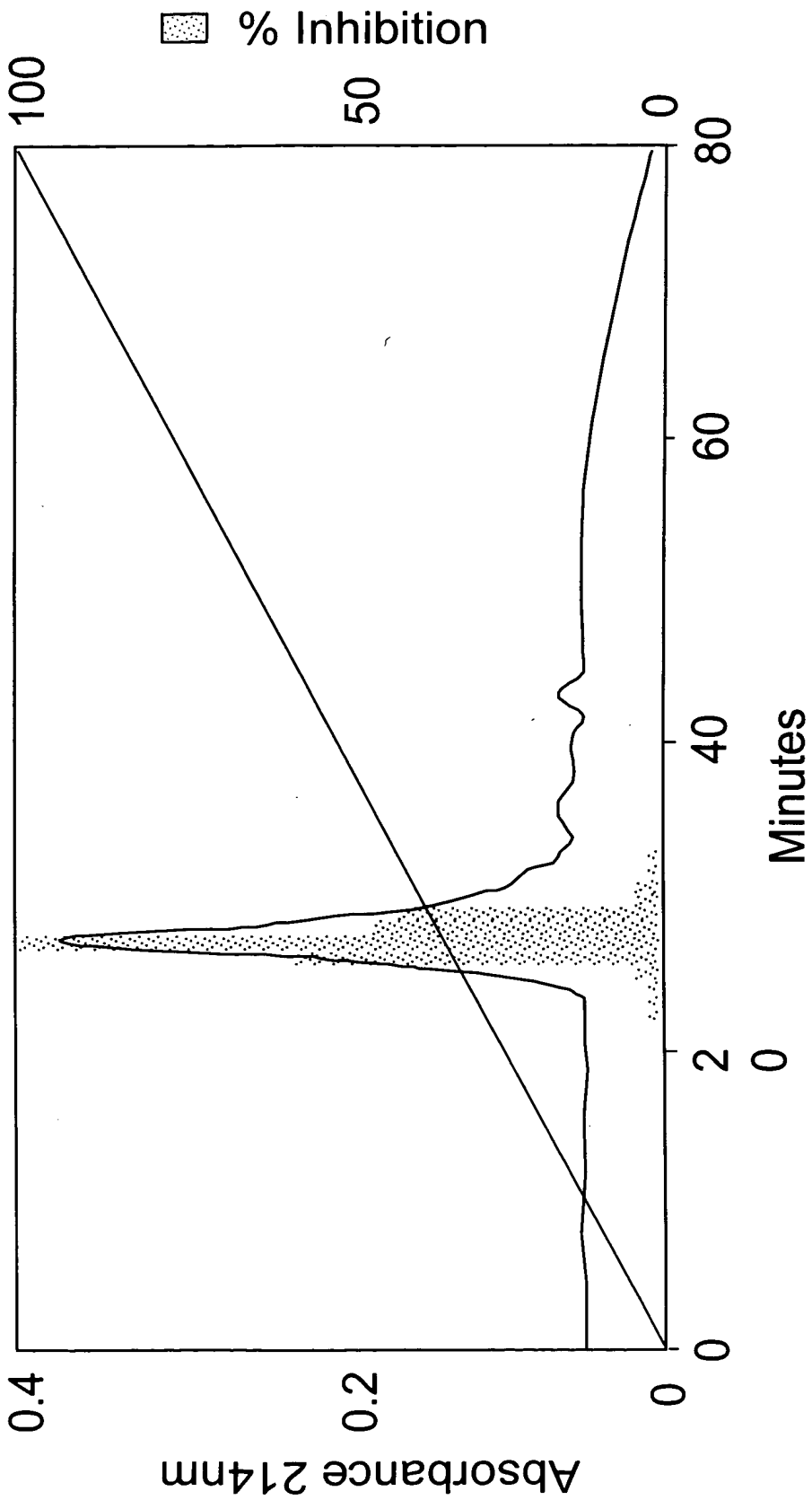
% Inhibition
100
50
0
80
60
40
2
0
Minutes
0.4
0.2
0
Absorbance 214nm

Fig. 3

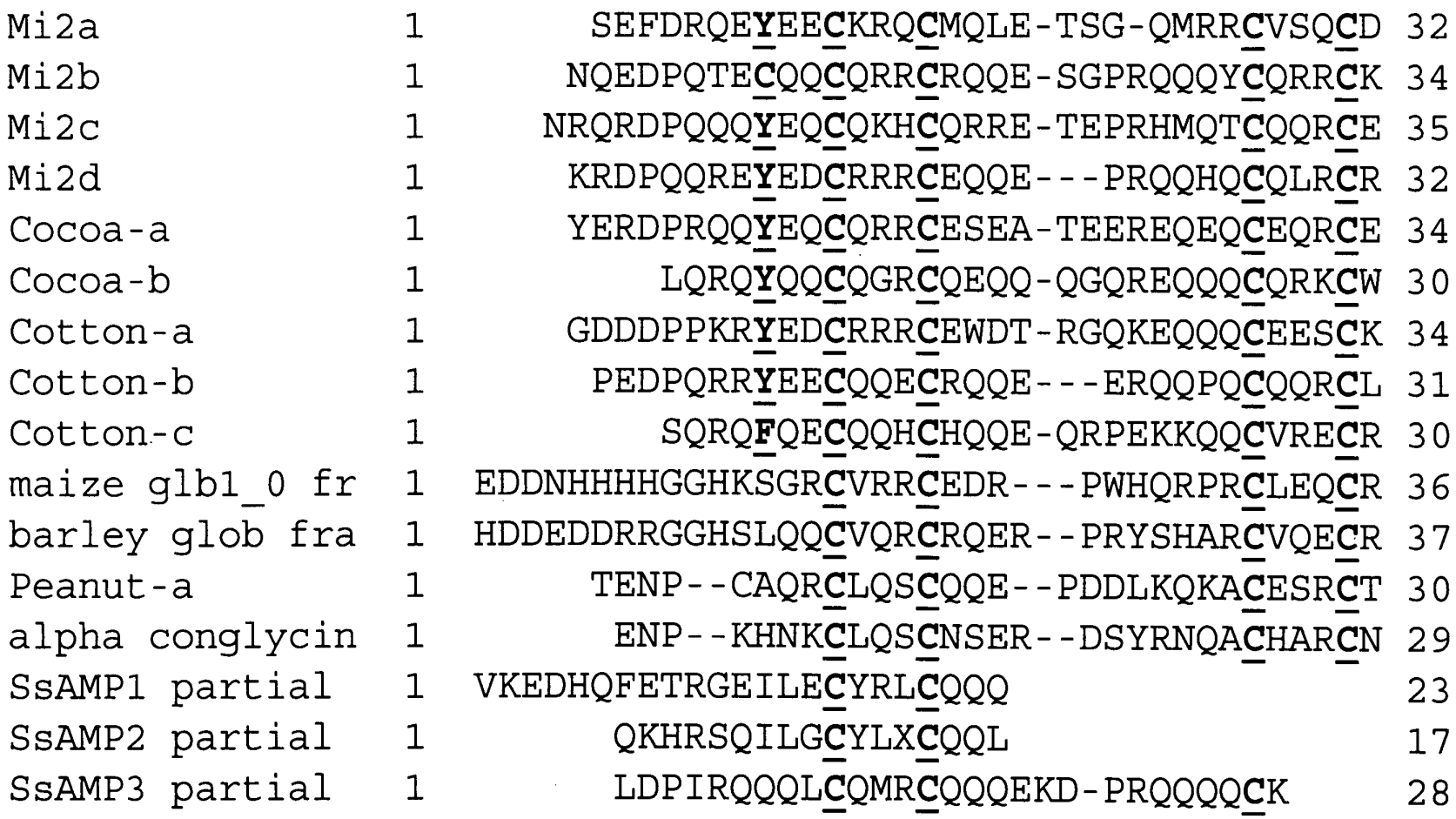
Mi2a 1 SEFDRQEYEECKRQCMQLE-TSG-QMRRCVSQCD 32
Mi2b 1 NQEDPQTECQQCQRRCRQQE-SGPRQQQYCQRRCK 34
Mi2c 1 NRQRDPQQQYEQCQKHCQRRE-TEPRHMQTCQQRCE 35
Mi2d 1 KRDPQQREYEDCRRRCEQQE---PRQQHQCQLRCR 32
Cocoa-a 1 YERDPRQQYEQCQRRCESEA-TEEREQEQCEQRCE 34
Cocoa-b 1 LQRQYQQCQGRCQEQQ-QGQREQQQCQRKCW 30
Cotton-a 1 GDDDPPKRYEDCRRRCEWDT-RGQKEQQQCEESCK 34
Cotton-b 1 PEDPQRRYEECQQECRQQE---ERQQPQCQQRCL 31
Cotton-c 1 SQRQFQECQQHCHQQE-QRPEKKQQCVRECR 30
maize glb1_0 fr 1 EDDNHHHHGGHKSGRCVRRCEDR---PWHQRPRCLEQCR 36
barley glob fra 1 HDDEDDRRGGHSLQQCVQRCRQER--PRYSHARCVQECR 37
Peanut-a 1 TENP--CAQRCLQSCQQE--PDDLKQKACESRCT 30
alpha conglycin 1 ENP--KHNKCLQSCNSER--DSYRNQACHARCN 29
SsAMP1 partial 1 VKEDHQFETRGEILECYRLCQQQ 23
SsAMP2 partial 1 QKHRSQILGCYLXCQQL 17
SsAMP3 partial 1 LDPIRQQQLCQMRCQQQEKD-PRQQQQCK 28

Fig. 4

Mi2a	33	KR**F**EEDIDWSKYD	45
Mi2b	35	EI**C**E**EEEEE**Y	43
Mi2c	36	RR**Y**EKEKRKQQKRYEEQQREDEEKYEERMK**EED**N	69
Mi2d	33	EQQRQHGRGGDMMNPQRGGSGRY**EE**G**EEE**QS	63
Cocoa-a	35	RE**Y**KEQQRQQ**EEE**	47
Cocoa-b	31	EQ**Y**KEQERGEHENYHNHKKNRS**EEEE**GQQR	60
Cotton-a	35	SQ**Y**GEKDQQQRHR	47
Cotton-b	32	KR**F**EQEQQQ	40
Cotton-c	31	EK**Y**QENPWRGER	42
maize glb1	37	EEEREKRQERSRHEADDRSGEGSS	60
barley glob	38	DDQQQHGRHEQEEEQGRGRGWHGEG**E**R**EE**	66
Peanut-a	31	KLEYDPR**C**VYDTGATNQRHPPGERT--RGRQP	60
alpha conglycin	30	LLKVEKEE**C**EEGEIPRPRPRPQHPER	55
SsAMP1 partial	23		23
SsAMP2 partial	17		17
SsAMP3 partial	28		28

Fig. 4 (continued)

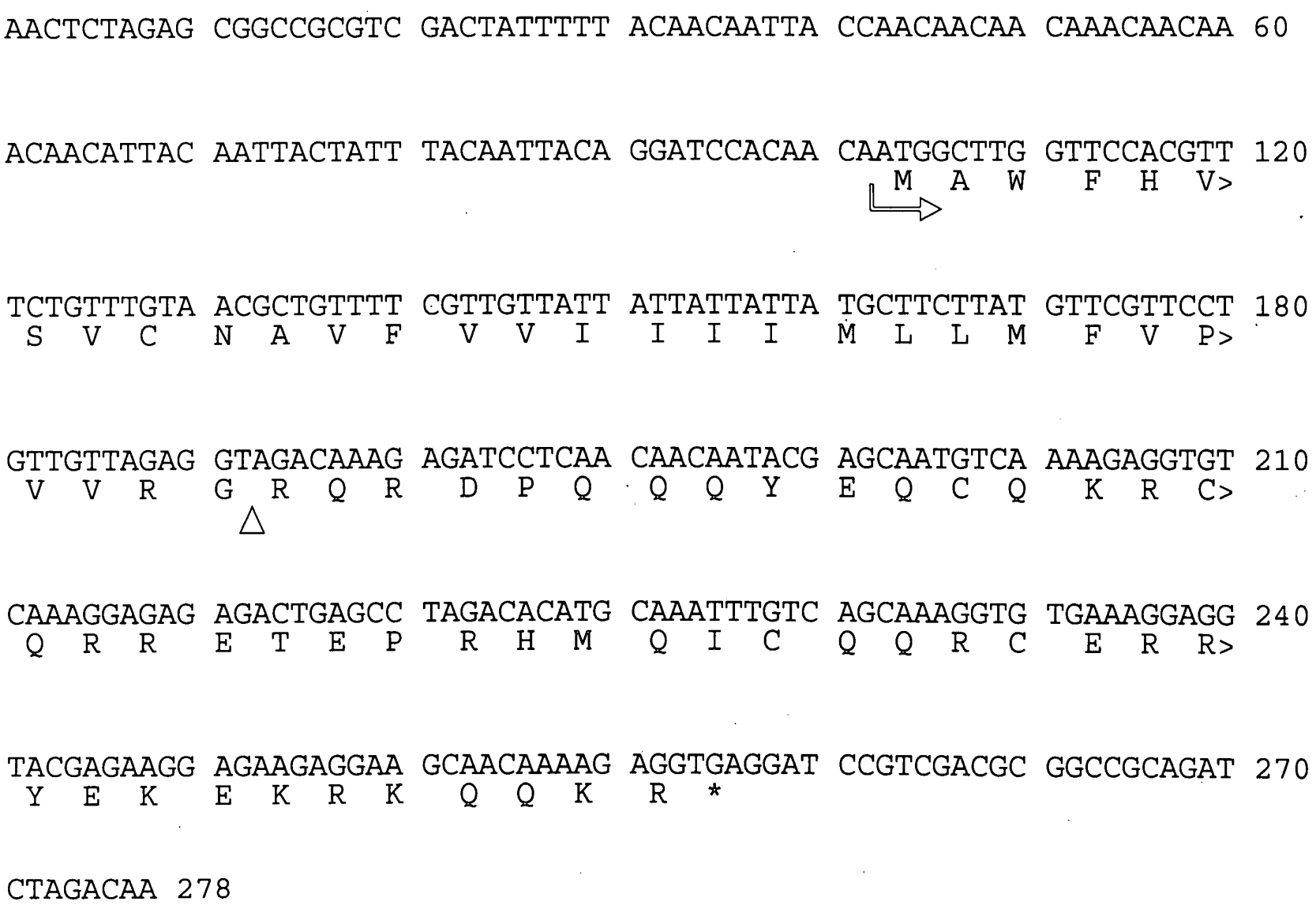
AACTCTAGAG CGGCCGCGTC GACTATTTTT ACAACAATTA CCAACAACAA CAAACAACAA 60
ACAACATTAC AATTACTATT TACAATTACA GGATCCACAA CAATGGCTTG GTTCCACGTT 120
M A W F H V>
TCTGTTTGTA ACGCTGTTTT CGTTGTTATT ATTATTATTA TGCTTCTTAT GTTCGTTCCT 180
S V C N A V F V V I I I I M L L M F V P>
GTTGTTAGAG GTAGACAAAG AGATCCTCAA CAACAATACG AGCAATGTCA AAAGAGGTGT 210
V V R G R Q R D P Q Q Q Y E Q C Q K R C>
CAAAGGAGAG AGACTGAGCC TAGACACATG CAAATTTGTC AGCAAAGGTG TGAAAGGAGG 240
Q R R E T E P R H M Q I C Q Q R C E R R>
TACGAGAAGG AGAAGAGGAA GCAACAAAAG AGGTGAGGAT CCGTCGACGC GGCCGCAGAT 270
Y E K E K R K Q Q K R *
CTAGACAA 278

Fig. 5

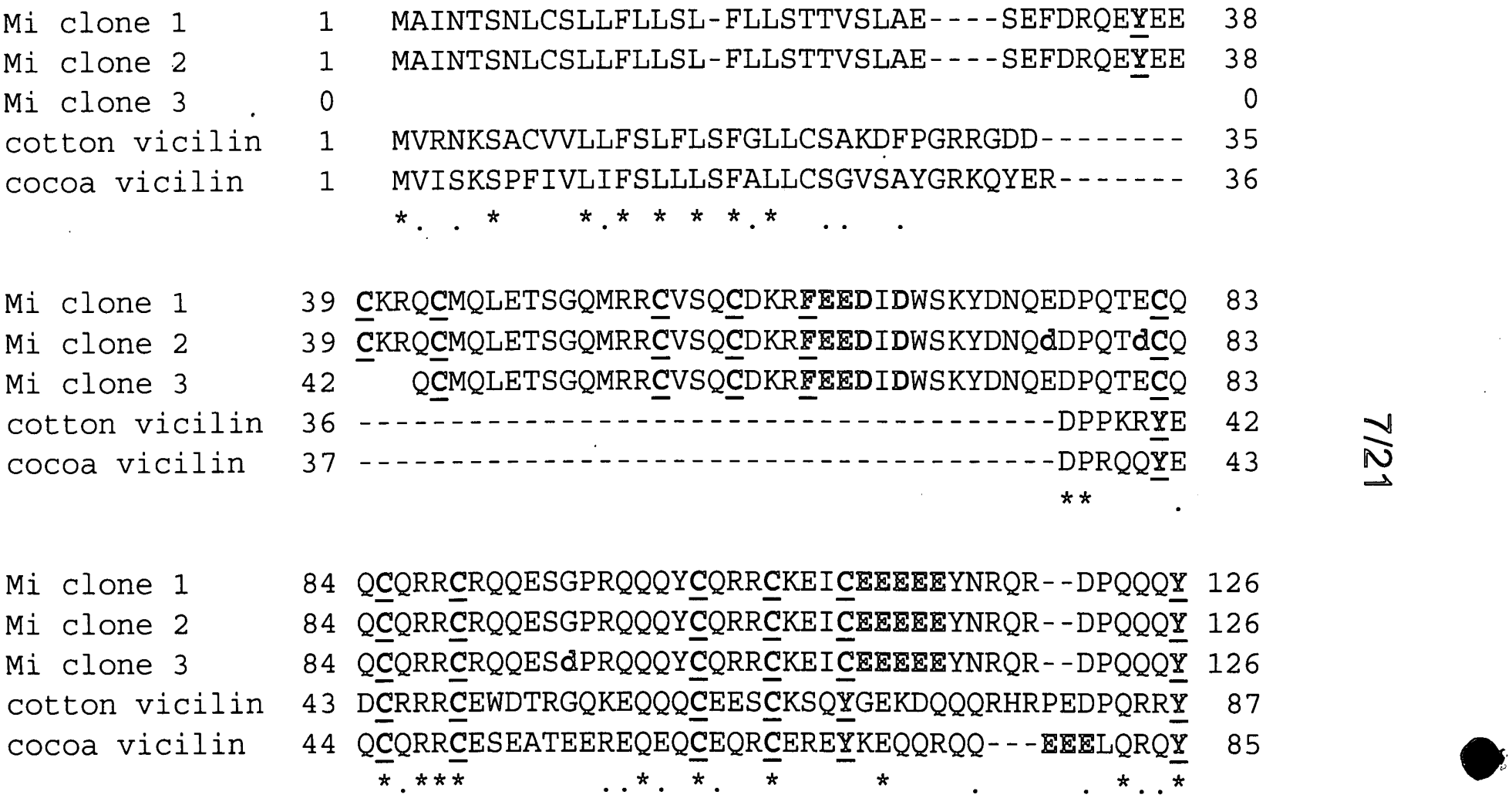
Mi clone 1 1 MAINTSNLCSLLFLLSL-FLLSTTVSLAE----SEFDRQEYEE 38
Mi clone 2 1 MAINTSNLCSLLFLLSL-FLLSTTVSLAE----SEFDRQEYEE 38
Mi clone 3 0 0
cotton vicilin 1 MVRNKSACVVLLFSLFLSFGLLCSAKDFPGRRGDD-------- 35
cocoa vicilin 1 MVISKSPFIVLIFSLLLSFALLCSGVSAYGRKQYER------- 36
Mi clone 1 39 CKRQCMQLETSGQMRRCVSQCDKRFEEDIDWSKYDNQEDPQTECQ 83
Mi clone 2 39 CKRQCMQLETSGQMRRCVSQCDKRFEEDIDWSKYDNQdDPQTdCQ 83
Mi clone 3 42 QCMQLETSGQMRRCVSQCDKRFEEDIDWSKYDNQEDPQTECQ 83
cotton vicilin 36 ----------DPPKRYE 42
cocoa vicilin 37 ----------DPRQQYE 43
Mi clone 1 84 QCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQY 126
Mi clone 2 84 QCQRRCRQQESGPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQY 126
Mi clone 3 84 QCQRRCRQQESdPRQQQYCQRRCKEICEEEEEYNRQR--DPQQQY 126
cotton vicilin 43 DCRRRCEWDTRGQKEQQQCEESCKSQYGEKDQQQRHRPEDPQRRY 87
cocoa vicilin 44 QCQRRCESEATEEREQEQCEQRCEREYKEQQRQQ---EEELQRQY 85

Fig. 6

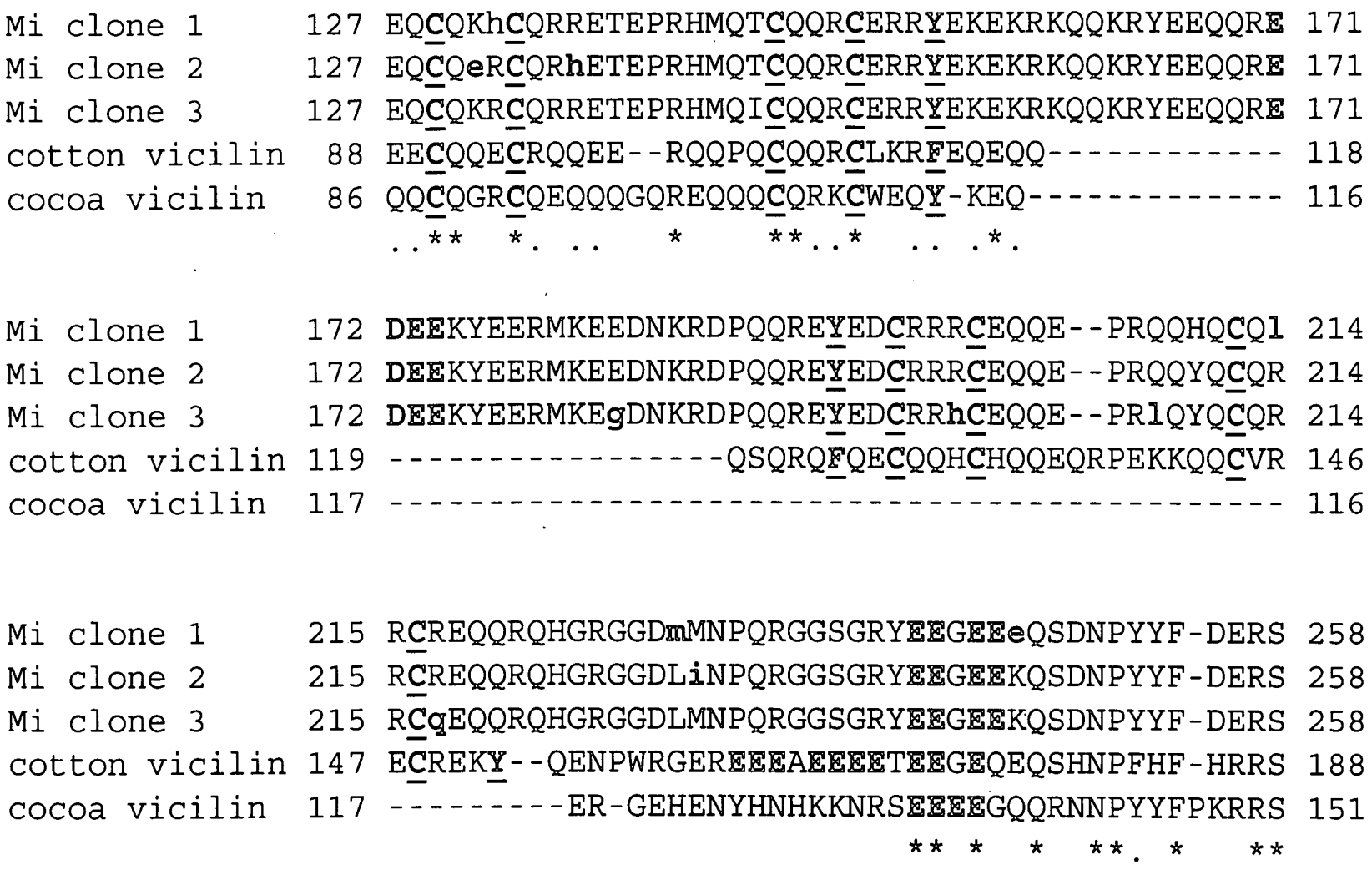

Fig. 6 (continued)

```
Mi clone 1      259 LSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVL 303
Mi clone 2      259 LSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVL 303
Mi clone 3      259 LSTRFRTEEGHISVLENFYGRSKLLRALKNYRLVLLEANPNAFVL 303
cotton vicilin  189 FQSRFREEHGNFRVLQRFASRHPILRGINEFRLSILEANPNTFVL 233
cocoa vicilin   152 FQTRFRDEEGNFKILQRFAENSPPLKGINDYRLAMFEANPNTFIL 196
                      .*** * *.  .*. *      *. .  .** . *****.*.*

Mi clone 1      304 PTHLDADAILLVIGGRGALKMIHhDNRESYNLECGDVIRIPAGTT 348
Mi clone 2      304 PTHLDADAILLVTGGRGALKMIHRDNRESYNLECGDVIRIPAGTT 348
Mi clone 3      304 PTHLDADAILLVIGGRGALKMIHRDNRESYNLECGDVIRIPAGTT 348
cotton vicilin  234 PHHCDAEKIYLVTNGRGTLTFLTHENKESYNIVPGVVVKVPAGST 278
cocoa vicilin   197 PHHCDAEAIYFVTNGKGTITFVTHENKESYNVQRGTVVSVPAGST 241
                    * * **. *  * .*.*..  . ..*.****.  * *. .***.*

Mi clone 1      349 FYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTF 393
Mi clone 2      349 FYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTF 393
Mi clone 3      349 FYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTF 393
cotton vicilin  279 VYLANQDNKEKLIIAVLHRPVNNPGQFEEFFPAGSQRPQSYLRAF 323
cocoa vicilin   242 VYVVSQDNQEKLTIAVLALPVNSPGKYELFFPAGNNKPESYYGAF 286
                     *.  .** *.* **     .  **..  ***** . *. *  .*
```

Fig. 6 (continued)

```
Mi clone 1      394 SKEILEAALNTQTEkLRGVf----GQQRE-GVIIRASQEQIRELT 433
Mi clone 2      394 SKEILEAALNTQaERLRGVL----GQQRE-GVIISASQEQIRELT 433
Mi clone 3      394 SKEILEAALNTQTERLRGVL----GQQRE-GVIIRASQEQIRELT 433
cotton vicilin  324 SREILEPAFNTRSEQLDELFGGRQSRRRQQGQG-MFRKASQEQIR 367
cocoa vicilin   287 SYEVLETVFNTQREKLEEILEEQRGQKRQQGQQGMFRKAKPEQIR 331
                    * *.**   **. *.*  .      ..*. *      .    ..

Mi clone 1      434 RDDSESRhWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPED 478
Mi clone 2      434 RDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPED 478
Mi clone 3      434 RDDSESRRWHIRRGGESSRGPYNLFNKRPLYSNKYGQAYEVKPED 478
cotton vicilin  368 ALSQEATSPREK-SGE--RFAFNLLSQTPRYSNQNGRFFEACPPE 409
cocoa vicilin   332 AISQQATSPRHR-GGE--RLAINLLSQSPVYSNQNGRFFEACPED 373
                       ..   . .  **  *   **  . * ***. *. .*  * .

Mi clone 1      479 YRQLQDMDlSVFIANvTQGSMMGPFFNTRSTKVVVVASGEADVEM 523
Mi clone 2      479 YRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEM 523
Mi clone 3      479 YRQLQDMDVSVFIANITQGSMMGPFFNTRSTKVVVVASGEADVEM 523
cotton vicilin  410 FRQLRDINVTVSALQLNQGSIFVPHYNSKATFVILVTEGNGYAEM 454
cocoa vicilin   374 FSQFQNMDVAVSAFKLNQGAIFVPHYNSKATFVVFVTDGYGYAQM 418
                    . * . . ..*    ..**..  * .*...* *. *. *    .*
```

Fig. 6 (continued)

```
Mi clone 1      524 ACPHLSGRHGGRGGGKRHEEEED-----VHYEQVRARLSKREAIV 563
Mi clone 2      524 ACPHLSGRHGGRrGGKRHEEEED-----VHYEQVkARLSKREAIV 563
Mi clone 3      524 ACPHLSGRHGGRGGGKRHEEEEE-----VHYEQVRARLSKREAIV 563
cotton vicilin 455 VSPHLPRQSSYEEEEEEDEEEEQEQEEERRSGQYRKIRSRLSRGD 499
cocoa vicilin  419 ACPHLSRQSQGSQSGRQDRREQEEESEEETFGEFQQVKAPLSPGD 463
                     .***  .          *.         . .   .

Mi clone 1      564 ---VLAGHPVVFVSSGNENLLLFAFGINAQNNHEN-----FLAGR 600
Mi clone 2      564 ---VpvGHPVVFVSSGNENLLLFAFGINAQNNHEN-----FLAGR 600
Mi clone 3      564 ---VLAGHPVVFVSSGNENLLLFAFGINAQNNHEN-----FLAGR 600
cotton vicilin 500 IFVVPANFPVTFVASQNQNLRMTGFGLYNQNINPDHNQRIFVAGK 544
cocoa vicilin  464 VFVAPAGHAVTFFASKDQPLNAVAFGLNAQN-----NQRIFLAGR 503
                        .  * * .*  . *    **.  **         *.**.

Mi clone 1     601 ERNVLQQIEPQAMELAFAAPRKEVEEsFNSQ-DqSIFFPGPRQHQQ 645
Mi clone 2     601 ERNVLQQIEPQAMELAFAAPRKEVEELFNSQ-DESIFFPGPRQHQQ 645
Mi clone 3     601 ERNVLQQIEPQAMELAFAAsRKEVEELFNSQ-DESIFFPGPRQHQQ 645
cotton vicili 545 INHVRQ-WDSQAKELAFGVSSRLVDEIFNSNPQES-YF-VSRQRQR 587
cocoa vicilin 504 --------- ----------------------PFFLNHKQNTN 514
                                                 .*  ..
```

Fig. 6 (continued)

Mi clone 1	646	QSPRSTKQQQPLVSILDFVGF	666
Mi clone 2	646	QS**s**RSTKQQQPLVSILDFVGF	666
Mi clone 3	646	QSPRSTKQQQPLVSILDFVGF	666
cotton vicilin	588	ASE	590
cocoa vicilin	515	VIKFTVKASAY	525

Fig. 6 (continued)

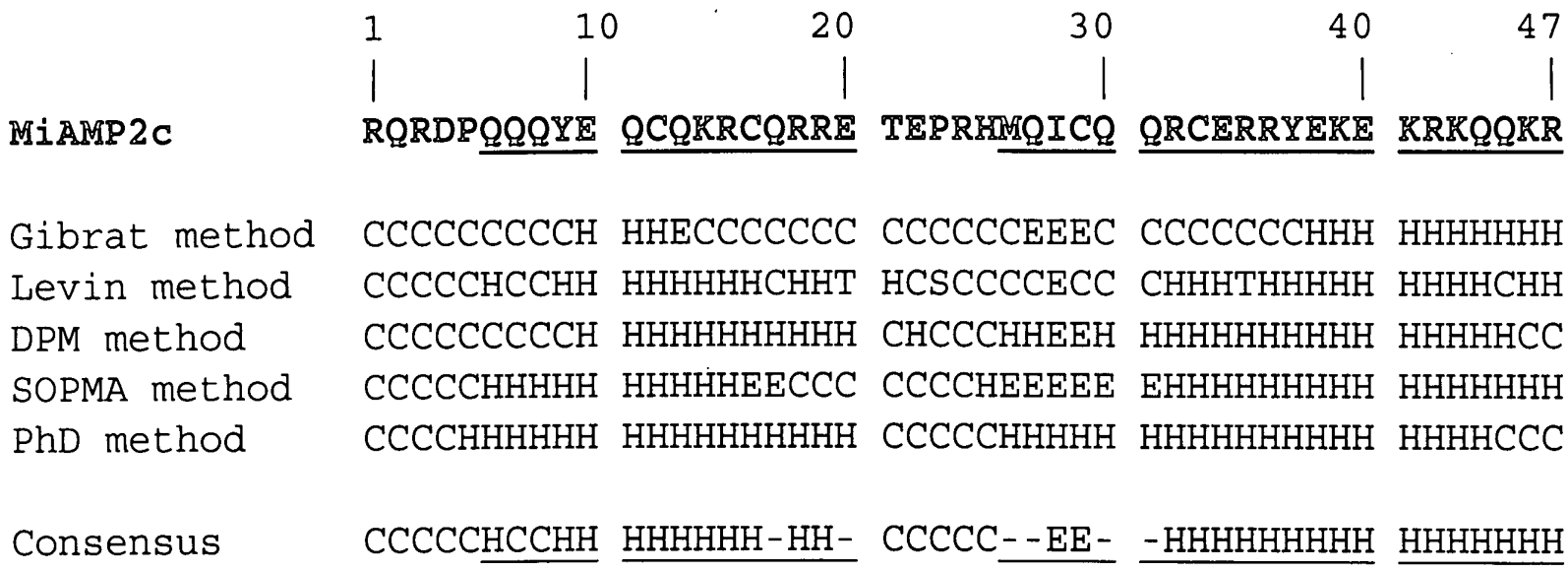
1 10 20 30 40 47
MiAMP2c RQRDPQQQYE QCQKRCQRRE TEPRHMQICQ QRCERRYEKE KRKQQKR
Gibrat method CCCCCCCCCH HHECCCCCCC CCCCCCEEEC CCCCCCCHHH HHHHHHH
Levin method CCCCCHCCHH HHHHHHCHHT HCSCCCCECC CHHHTHHHHH HHHHCHH
DPM method CCCCCCCCCH HHHHHHHHHH CHCCCHHEEH HHHHHHHHHH HHHHHCC
SOPMA method CCCCCHHHHH HHHHHEECCC CCCCHEEEEE EHHHHHHHHH HHHHHHH
PhD method CCCCHHHHHH HHHHHHHHHH CCCCCHHHHH HHHHHHHHHH HHHHCCC
Consensus CCCCCHCCHH HHHHHH-HH- CCCCC--EE- -HHHHHHHHH HHHHHHH

Fig. 7

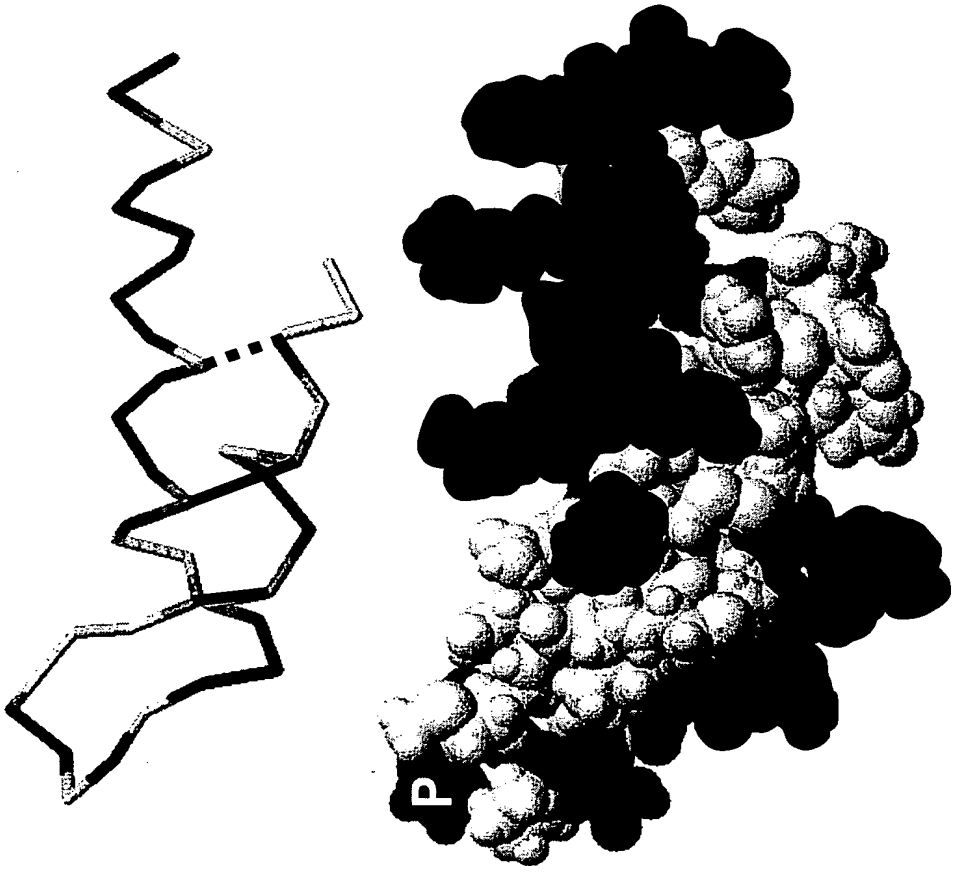

Fig. 8

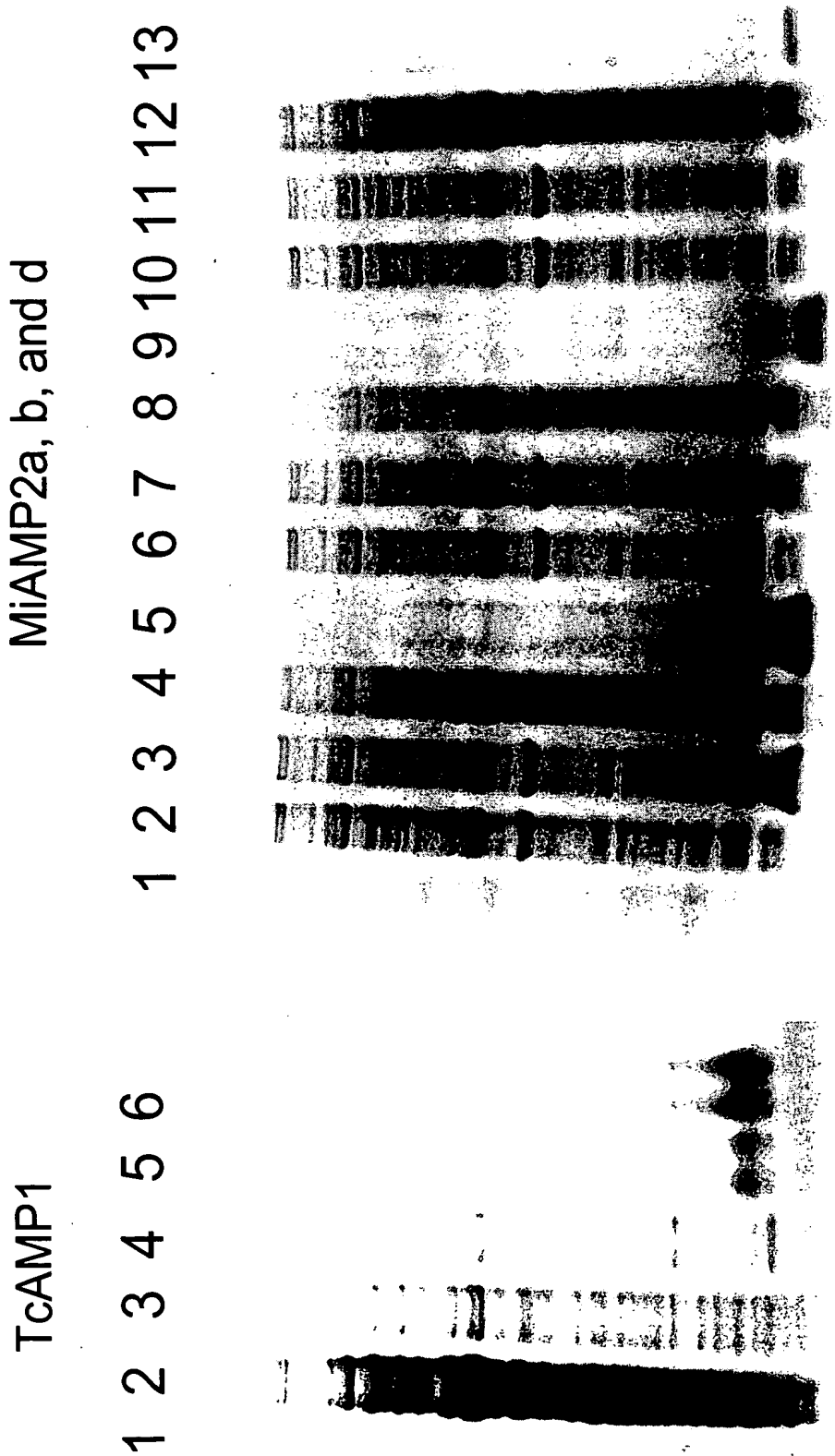

Fig. 9

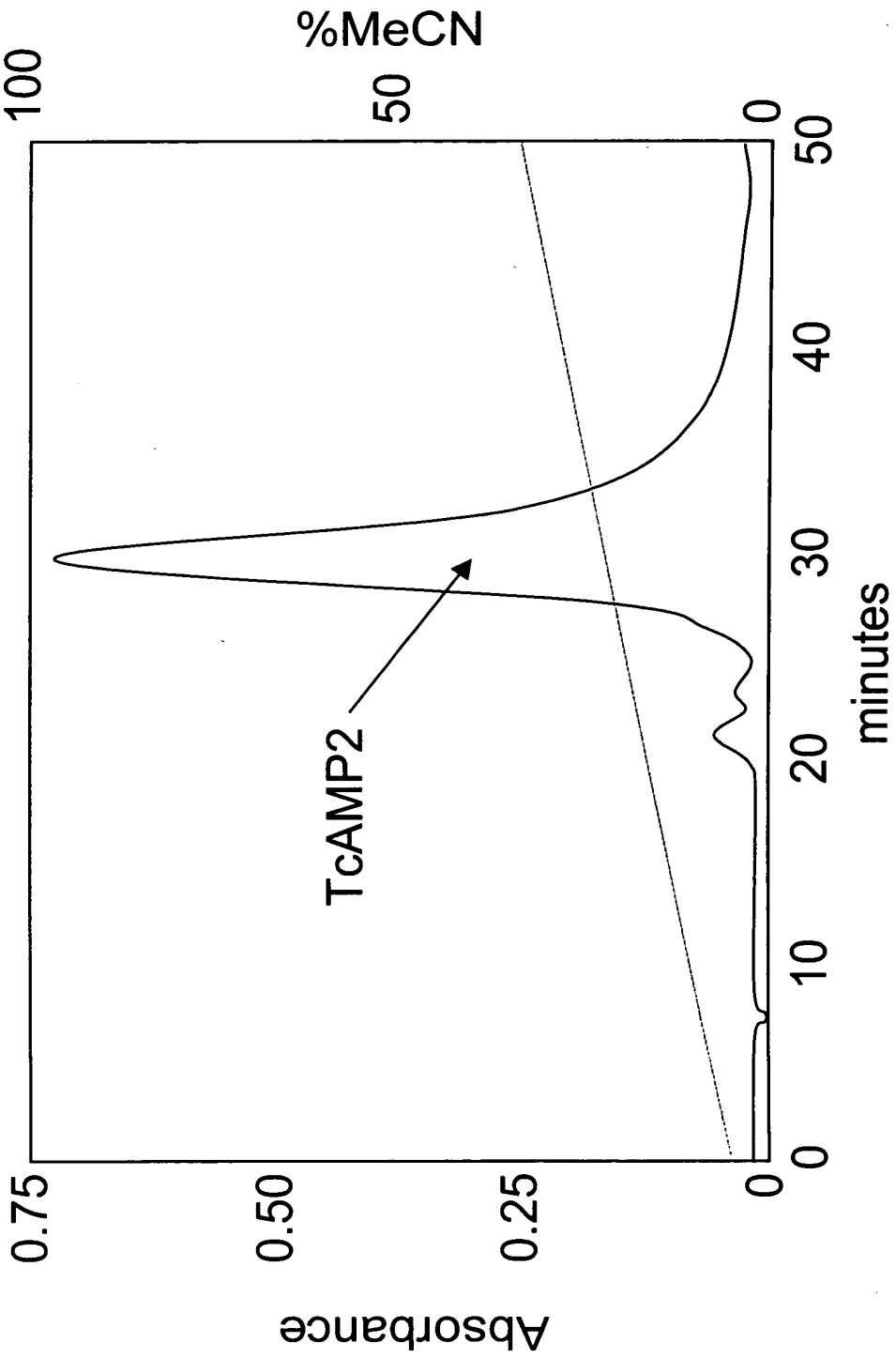
%MeCN
100
50
0
Absorbance
0.75
0.50
0.25
0
0
10
20
30
40
50
minutes
TcAMP2

Fig. 10

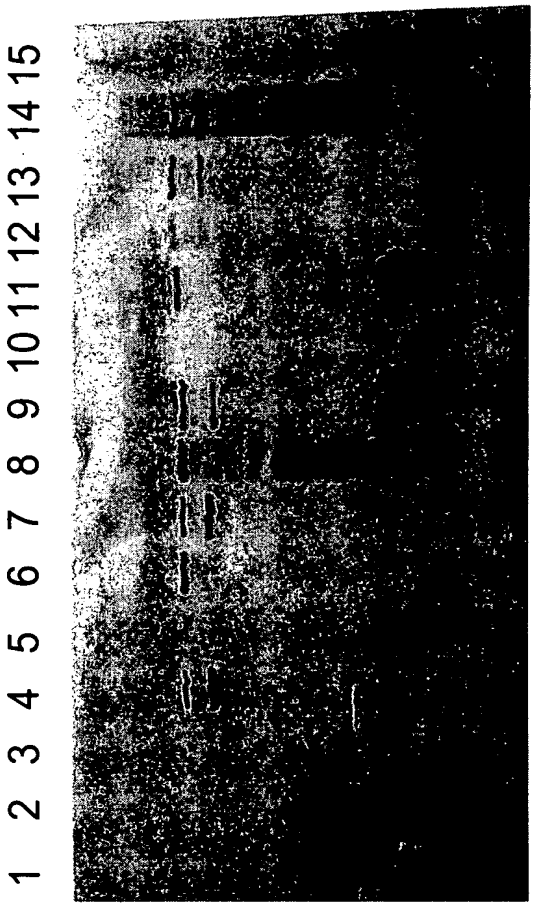

Fig. 11

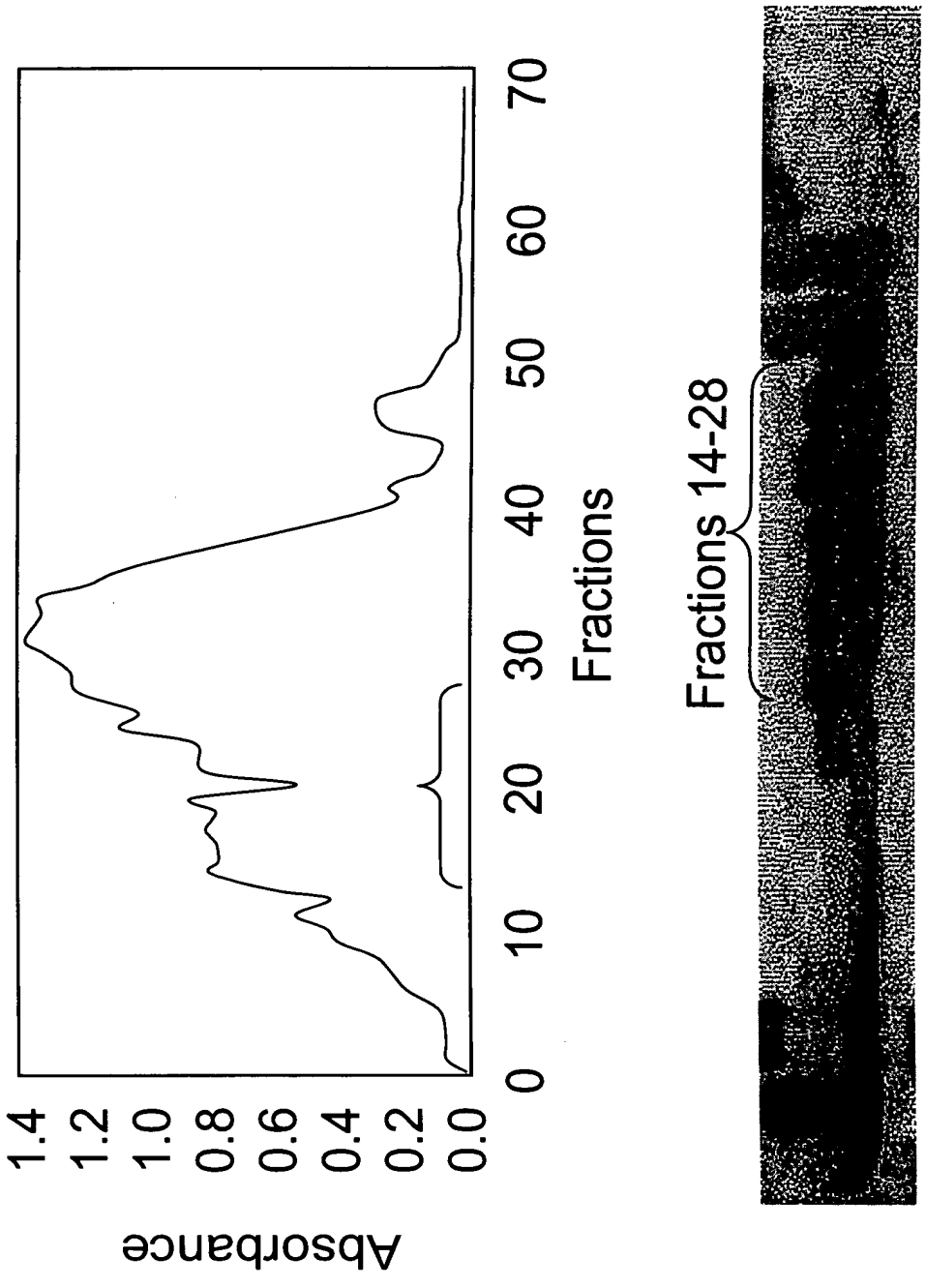
Absorbance
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
10
20
30
40
50
60
70
Fractions
Fractions 14-28

Fig. 12

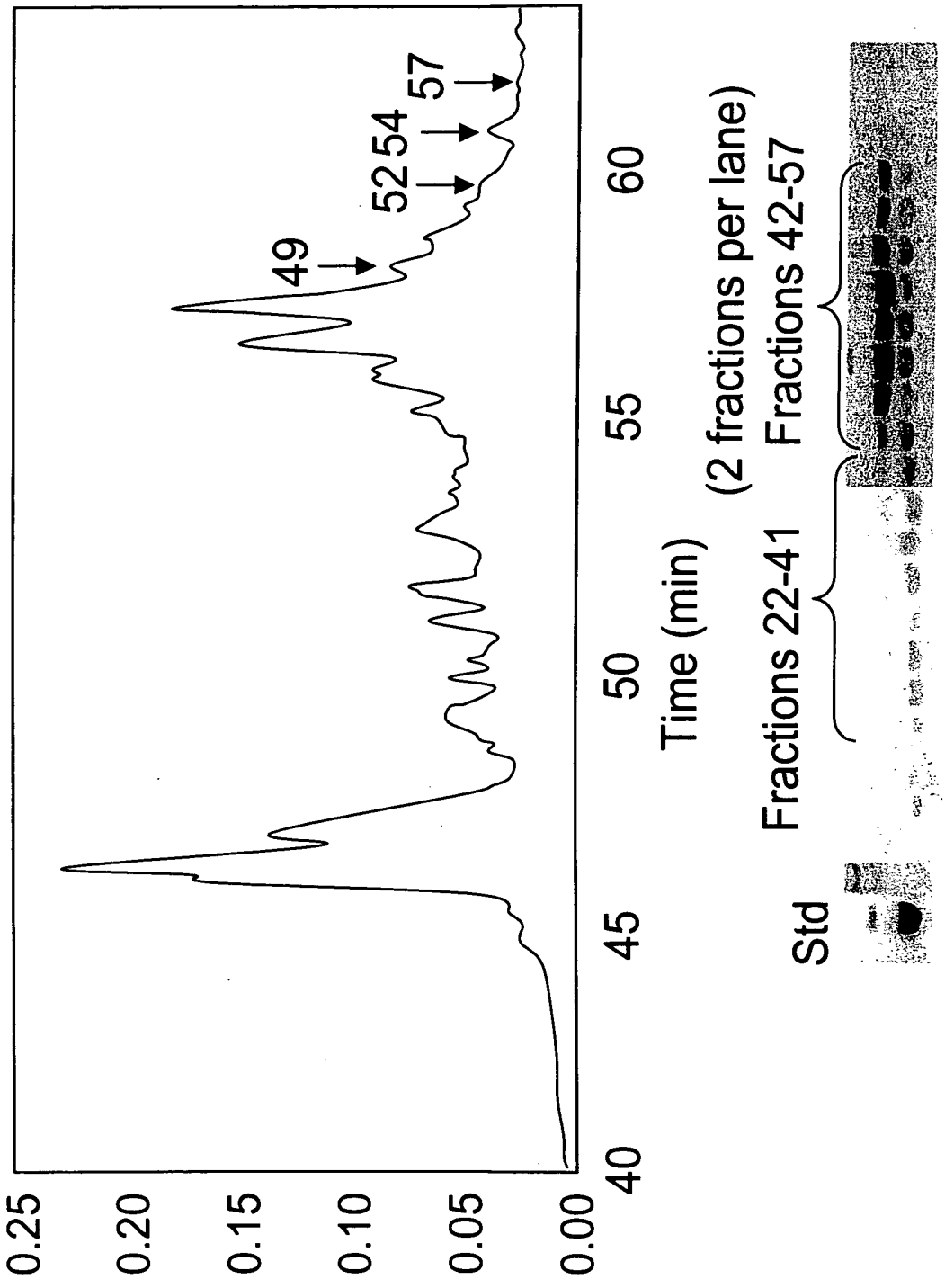
0.25
0.20
0.15
0.10
0.05
0.00
40
45
50
55
60
Time (min)
49
52
54
57
Std
Fractions 22-41
(2 fractions per lane)
Fractions 42-57

Fig. 13

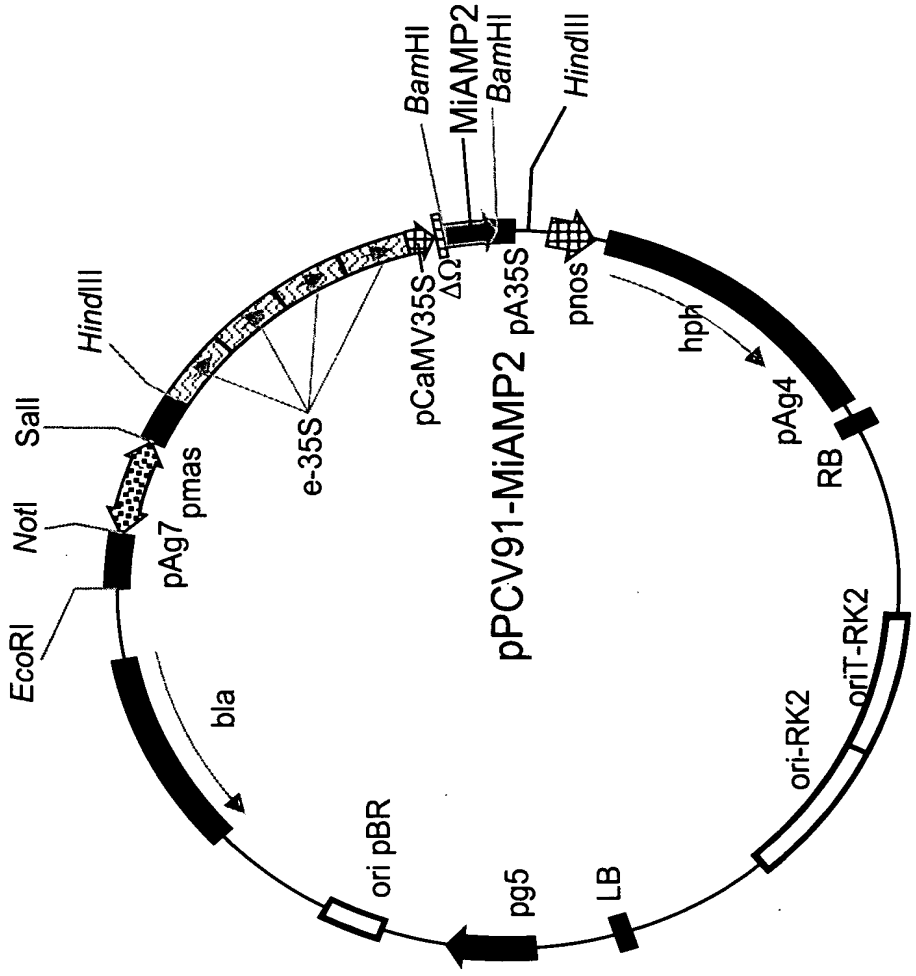
pPCV91-MiAMP2
BamHI
MiAMP2
BamHI
HindIII
pCaMV35S
ΔΩ
pA35S
pnos
hph
pAg4
RB
oriT-RK2
ori-RK2
LB
pg5
ori pBR
bla
EcoRI
NotI
pAg7
pmas
e-35S
HindIII
SalI

Fig. 14

Fig. 15